

FIGURE 144

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTGGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT
GGAGGGACAGGGTCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGACAGGGCGTTGGG
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCTCGAGC
GCTGGTACTCTGGGCTGCACTGGGGGACAGAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACCTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCTGCCTGCACCCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCGGCTGCT
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACAGGGCTTCTCTGCTG
AGGTGCAGCTCATTCACTTCAACCAGGAACCTCTACGGGAATTTACAGCGCTGCCTCCCGCGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCTC
CAGTGCCTCCTTAACCGCGACACCATCACTCGCATCTCTACAAGAATGATGCCTACTTTT
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC
TCTCTCAGACCCCGCCTGCTCCGAGACTGTACCTGGATCCTCATTGACCGGGCCCTCAA
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCTCCATCTCAGATCT
TCCAGAGCCTCAGCGGTAACAGCCGGCCCTGCAGCCCTTGGCCCCACAGGGCACTGAGGGG
AACAGGGACCCCCGCGACCCCGAGAGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGA
TGGTGTCCCCATGGTGCCTGAGACTCCCTTCGAGGATTGCACCCGCGCCGTCCTAAGCCTC
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

097366.10464

FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop .

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTRHVSFLPAPRPVVNVSGGGL
LYSHRLSELRLFLGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVAASNPFSLRLLNRDTITRISYKNDAFLQDLSELELFPESFGFITYQGSLSLTPPCSE
TVTILIDRALNITSLQMHSLRLLSQNPSPQIFQSLSGNSRPLQPLAHRALRGNRDPRHPR
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

007325.14501
10522.56266

FIGURE 146

GGCGCCTGGTTCCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCCGCCGCCAGCCTC
 GTTCGTGTCCCGCCCTCTCGCTCTGTCAGCTACTGCTCAGAAACGCTGGGGCGCCACCCTCTGGCAGACTAACGAA
 GCAGCTCCCTTCCCAACCCCACTGCGAGTCTAATTTTGGACGCTTTGGCTGACCAITTTCTCCAGGTTTGGGGAGC
 CGCAGAGGCGGAGGCTCGGTATTTCTGTCAGTCAGCACCCACGTCGCCCGCCGAGCGCTCGGTGTCTCAGGCCCTTC
 GCGAGCGGGGCTCTCTCGTCTGCGGTCCTTTGTGAAGGCTCTGGGCGGCTGCGAGAGCCGGCCGCTCGGTTTGGCT
 CACCTCTCCCAGGAACTTCACTGGAAGAGCCAAAGGAGTGAAGAGCCTGCTCTTGGAGATTTTCTGGGGAA
 ATCTCAGGTCAITCAATATGAAGTGATACCGCGCGGAGTGGCTCAGAGTAAACCAAGTGGCTGTTCATGGCTAGA
 GCAATTCAGGCCATGGTGGTCCCAATGCCACTTTATTTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT
 GAGTGGTGGTGGGCAAAACAGAGGGGAAAGGGCCATCACAGACAATGACATGCGAGATATTTTGGACCTTCAT
 AATAAATACGAAGTCAAGTGTATCCACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
 TCTCAGAAATCTGGGCTGAAAGTTGCTTTGTGGAAACATGGACCTGCAAGCTTGCTTCCATATGGACAGAAT
 TTTGGGAGCACACTGGGGAAGATATAGGCCCGGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAGACTTT
 AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTGAGTGTCTGGCCCTGTATGTAACATTATACA
 CAGGTCGTGGGCAACTAGTAAACGAATCGGTTGTGCCATTAAATTTGTGTACATAACATGAACATCTGGGGCGAG
 ATATGGGCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCAAGGGAAACTGTTGGGGCCATGCCCTTACAAA
 CATGGGCGGCCCTGTTCTGCTTGGCCCACTAGTTTGTGGAGGGGCTGTAGAGAAATCTGTGCTACAAAGAGGG
 TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAATAGAACGACAGCAGTCACAAGTCCATGACACC
 CATGTCCGACAGATCAGATGATAGTACAGAAATGAAGTCAATAGCGCACAGCAATGTCCCAATATGTTTCT
 TGTGAAGTAAATTAAGAGATCAGTGCAGAGGAAACCACTGCAATAGGTACGAATGTCTGCTGGCTGTTTGGAT
 AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAATGCAATCCAGCATCTGTAGAGCTGCAATTCTATTATGGT
 ATATAGACAAATGATGTTGGCTGGTATGATACATGACAGAGGAAAGAGCATTTTCTCAAGTCCATGATGA
 AATGGTATTCAAAGTAAATATCAGTCTGCTAATTTCTTCCAGCTCTCAAAGTAAAGTACAGTTCAGGCTGTG
 ACTTTGTGAAACCACTGTGGAAACAGCTCTGTCCATTTCATATAGCCTGCTCTTCAAGTGTCCCAAGATATATCTGCT
 CGTAACTGTATGTCAGCAAAATCAGCATATGCTGTGTAAATGGAACTCGAGTTTATTCTGATGTGTCAGTATC
 TGCAGAGCAGCAGTACATGCTCGGAGTGGTTCCGAAATCAGGTCGTTATGTTGATGTAAATGCTCTGGAGCAAAAG
 AAGACCTACATTGCTCTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAACTCTCCAGGAGGAAAGGCCATT
 AGAGTGTGTTGCTGTTGTGGAAGTAACTTGGGAAGGAGGACATAAAGACTATTCCAAATGCAATATTTCTGA
 ATTTTGTATAAACTGTAACTATCTGTACAGAGTACATCAACTATTTTCCAGCCAAAAAGGTGCCAAATGCATA
 TAAATCTGTATAAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTTGGGAAAAAGTAAATGAAAATATAATGG
 TTTTGAAGATCCTGTGTTAAATATTGCTATATTTTCTAGCAGTATTTTCTACAGTAAATACATAGTCATGATT
 GTTCTACGTTTCATATATATATGTTGCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAAT
 GCCCTCAGAAAAATCATCTAGTGCAATTAAAAATAATCGACTCTAAAACTGAAAGAAACCTTATCACTTTTCCCC
 AGTTCAATGCTATGCCATTACCAACTCCAAATATCTCAATATATTTTCCACTTAAATACTGTAAGGTTTTTTTT
 GTTAAATTTAGGCATATAGAAATATTAATCTCGATATTGCACTTCTTATTTTATATAAAAAATCTCTTAAATATC
 CAAATGAATCTGTTAAAAATGTTGATTCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT
 ATGAAAAACATCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTCTATGTACTGTTA
 AAATTGAGGTACATATTTTCTTTTGTATCTGGCAAATACTCCTGCAGGCGCAGGAGTATAATAGCAAAAAAGTT
 GAACAAAGATGAACATAATGATATACATTACCAATTGCCACTGATTTTAAAAATGTTAAATGACCTTTGATATAA
 ATATTGCCATATCATGGTACCTATAATGGTGATATATTGTTTCTATGAACAAATGATATTGCTTTGATACATAAA
 AATCTGTAAAAATGTTAGTTTGGTAAATTTTCTTCTGCTGGTGGATTACATTAATAATTTTCTGCTGGTGGGA
 TAAACATTAAAAATTAATCATGTTTCAAAAAA

03673295-103504